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Microbial Monitoring-Based Health Management Models for Marine Aquaculture

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Abstract Marine aquaculture is moving toward greater production intensity while facing persistent challenges from infectious disease, environmental instability, and antimicrobial resistance. In this setting, microbial communities should no longer be treated only as a background component of the culture environment. They participate in nutrient cycling, organic matter transformation, host nutrition, mucosal defense, pathogen exclusion, and disease development. This review examines how microbial monitoring can be translated from a descriptive research tool into a practical component of marine aquaculture health management. Conventional culture, PCR-based assays, 16S rRNA gene sequencing, metagenomics, multi-omics approaches, flow cytometry, biosensors, and field-deployable molecular methods provide complementary information at different levels of taxonomic, functional, quantitative, and temporal resolution. Particular attention is given to potential pathogens, health-associated microorganisms, community stability, dysbiosis, and functional genes as candidate indicators. Current evidence indicates, however, that no single microbial taxon or diversity metric can serve as a universal marker of health. Monitoring is most informative when microbial signals are interpreted against farm-specific baselines and integrated with water quality, production stage, and host-health observations. On this basis, the review proposes a tiered framework linking routine surveillance, early warning, risk classification, proportionate intervention, and post-intervention feedback. The framework intentionally avoids fixed universal thresholds because microbial communities vary substantially among species, farms, seasons, and production systems. Future progress will depend on standardized sampling, absolute microbial quantification, longitudinal and multi-farm validation, functional confirmation of biomarkers, and integration of rapid microbial monitoring with environmental sensors and data-driven decision support. Microbial monitoring can therefore support a gradual shift from reactive treatment of disease toward preventive, adaptive, and precision health management in sustainable marine aquaculture.

Keywords Marine aquaculture; Microbial monitoring; Microbiome; Microbial dysbiosis; Health management; Disease early warning; Microbial indicators; Sustainable aquaculture

1 Introduction

Aquaculture has become increasingly important to global aquatic food production, and its continued expansion is central to meeting demand for aquatic foods without relying solely on capture fisheries. The Food and Agriculture Organization reported that aquaculture surpassed capture fisheries in aquatic animal production in 2022, highlighting both its growing contribution and the need to improve biological and environmental sustainability. Intensification, however, concentrates animals, feed inputs, organic matter, and microorganisms within comparatively restricted environments. Disease remains one of the major biological constraints on aquaculture, while environmental change, pathogen transmission, and antimicrobial resistance complicate conventional health management (Naylor et al., 2021).

Traditional aquatic animal health management has largely focused on recognizable pathogens: detect the causative agent, confirm disease, and then intervene. Such a strategy remains essential during outbreaks, but it is inherently reactive. It may also overlook the ecological transition that occurs before obvious clinical signs appear. International aquatic animal health guidance increasingly combines disease control with biosecurity, surveillance, prevention, and responsible antimicrobial use rather than relying on treatment alone. At the farm level, the unresolved question is how to recognize a deteriorating biological state early enough for low-impact intervention to be useful.

Microbial ecology offers a way to address this gap. An aquaculture animal lives within a connected microbial landscape comprising the surrounding water, sediment, tank or cage surfaces, feed, biofilms, and microorganisms associated with the gut, gills, skin, and mucus. These assemblages are not static. They respond to animal development, temperature, salinity, nutrient loading, husbandry, disease, and treatment. In a 13-month survey of Sanggou Bay mariculture, for example, seasonality strongly structured bacterioplankton communities, while potentially pathogenic *Vibrio* became more prominent during late-summer and autumn high-risk periods (Lu et al., 2025). Longitudinal studies in fish, shrimp, and hatchery shellfish similarly show that temporal context is indispensable when microbiomes are interpreted as health indicators (Cram et al., 2024; Bui et al., 2026).

The concept of microbial dysbiosis extends this perspective beyond pathogen abundance. Dysbiosis refers to an unfavorable departure from a host- or system-associated microbial state and may include community restructuring, loss of potentially protective organisms, proliferation of opportunists, altered interactions, or changed microbial functions. Reviews of aquaculture microbiomes have proposed such changes as potential disease biomarkers, while also warning that a universal "healthy microbiome" has not yet been defined (Infante Villamil et al., 2021; Mougin and Joyce, 2023). The distinction matters: a microbial change can precede disease, result from disease, or simply reflect a normal environmental transition.

Technological advances make this ecological information increasingly accessible. Targeted qPCR and digital PCR provide sensitive quantification; 16S rRNA sequencing reveals broad community structure; shotgun metagenomics can recover genes and genomes; metabolomics and transcriptomics add functional information; and rapid approaches such as flow cytometry and isothermal amplification shorten the interval between sampling and interpretation. Field-oriented LAMP assays for marine *Vibrio* illustrate how molecular detection is beginning to move from specialized laboratories toward farm-side surveillance (Rahman et al., 2022; Pu et al., 2026).

The purpose of this review is therefore not to present microbiome sequencing as a replacement for veterinary diagnosis, water-quality monitoring, or conventional biosecurity. Rather, it examines how microbial information can be integrated with those practices to create a more anticipatory health-management system. The discussion moves from microbial ecology and monitoring technologies to candidate health indicators, environmental drivers, early-warning strategies, practical management models, and applications across major marine aquaculture systems. The central argument is that the greatest value of microbial monitoring lies not in identifying a universal "good" or "bad" bacterium, but in detecting meaningful deviations from a well-characterized biological baseline early enough to support proportionate management.

2 Microbial Communities and Health in Marine Aquaculture Systems

2.1 Composition and ecological functions of microbial communities

Marine aquaculture systems contain overlapping but non-identical microbial habitats. Water-column communities respond rapidly to temperature, nutrient availability, phytoplankton, dissolved organic matter, and hydrodynamics, whereas sediment and biofilm communities experience stronger gradients in oxygen and organic loading. Host-associated communities add another level of selection because the gut, gills, skin, and mucus provide distinct physicochemical conditions. Even within a single shrimp, gastrointestinal compartments can contain different community structures, emphasizing that "the microbiome" is not one uniform biological compartment (Garibay-Valdez et al., 2021).

These microorganisms collectively contribute to organic matter degradation and carbon, nitrogen, and sulfur transformations while competing, cooperating, and exchanging metabolites with one another. In biofloc shrimp systems, rearing-water communities show clear succession during the production cycle, with different bacterial groups becoming prominent at different stages (Kim et al., 2022). Metagenomic comparison of grouper cage waters and nearby non-aquaculture waters has likewise linked aquaculture-related nutrient enrichment with shifts in both microbial composition and predicted biogeochemical functions (Liu et al., 2024).

2.2 Host-Microbiome interactions in cultured marine animals

Host-associated microbiota occupy interfaces where nutrition, immunity, and environmental exposure meet. Gut microorganisms can participate in nutrient transformation and production of metabolites, while mucosal communities on the skin and gills interact directly with host defenses and incoming environmental microorganisms. Research across fish increasingly supports the view that host identity, development, environment, and diet jointly structure these communities rather than one factor acting independently (Yajima et al., 2023; Zhao et al., 2023).

A protective microbiome should nevertheless be understood functionally rather than as a fixed list of beneficial taxa. Some resident organisms may occupy niches that would otherwise be available to pathogens, produce antagonistic compounds, or influence mucosal immune responses. Conversely, a normally harmless member may become problematic when environmental conditions or host defenses change. This context dependence is especially important in aquaculture, where the same bacterial genus may contain commensal, probiotic, and pathogenic strains. Consequently, genus-level sequence data should rarely be interpreted as direct evidence of disease or protection (Mougin and Joyce, 2023).

2.3 Microbial homeostasis and dysbiosis

Microbial homeostasis is better described as a resilient range than a constant community composition. A healthy animal or production system can undergo substantial temporal turnover while retaining important ecological functions. Atlantic salmon gill communities, for example, restructure through the marine production cycle, and not every change in richness or diversity corresponds to poorer gill health (Clinton et al., 2024). This finding argues against using a single diversity index as a universal health threshold.

Dysbiosis becomes more informative when several signals converge: abrupt community turnover, enrichment of opportunists, loss of persistent host-associated taxa, altered network structure, functional changes, and measurable deterioration of host or environmental condition. In shrimp white feces syndrome, experimental work provided evidence that altered intestinal microbiota can contribute to disease processes rather than merely reflect them (Huang et al., 2020). Yet causality should not be assumed in every system. Oyster hatchery research has shown that some microorganisms enriched during production crashes appear to proliferate after host deterioration rather than initiate it (Cram et al., 2024).

3 Microbial Monitoring Technologies for Marine Aquaculture

3.1 Conventional microbial monitoring methods

Culture-dependent microbiology remains useful because isolates can be phenotyped, tested for pathogenicity or antimicrobial susceptibility, preserved, and examined experimentally. Selective media and colony enumeration are relatively inexpensive and provide information on culturable populations that molecular surveys alone cannot deliver. Their principal weakness is incomplete coverage: many environmental microorganisms are difficult to culture under routine laboratory conditions, while culture and biochemical identification may take longer than desirable during rapidly developing disease events (Rahman et al., 2022).

The most practical strategy is therefore complementary rather than competitive. Culture is particularly valuable when an isolate is required for challenge testing, antimicrobial susceptibility, genomic characterization, or probiotic development; sequence-based and molecular methods are better suited to broad surveillance and rapid detection. Maintaining this distinction prevents the common error of treating a DNA sequence as equivalent to a viable pathogenic organism.

3.2 Molecular detection of target microorganisms

PCR and qPCR transformed pathogen surveillance by allowing specific microbial targets to be detected without lengthy cultivation. qPCR additionally estimates target abundance, making it more useful for longitudinal monitoring than simple presence/absence testing. Digital PCR partitions reactions and can provide absolute nucleic-acid quantification without a conventional calibration curve. In seawater experiments, a propidium-monoazide–ddPCR approach was able to distinguish viable-target DNA from dead-cell DNA for toxigenic *Vibrio cholerae*,

illustrating how viability and absolute quantification can be incorporated into environmental surveillance (Yang et al., 2023).

The limitation of targeted assays is equally clear: they detect what investigators decide to search for. A well-designed qPCR panel can be highly useful when key pathogens and virulence markers are known, but it cannot describe an unexpected community-wide shift. For health management, targeted PCR is therefore best positioned as a rapid confirmation layer within a broader monitoring program.

3.3 16S rRNA gene amplicon sequencing

16S rRNA gene sequencing remains one of the most accessible approaches for characterizing bacterial and archaeal communities. It can compare alpha diversity, community dissimilarity, taxonomic composition, succession, and candidate indicator taxa across time, farms, tissues, or health states. Longitudinal shrimp, salmon, oyster, and barramundi studies demonstrate how these profiles can reveal microbial changes that are invisible to routine culture or single-target assays (Kim et al., 2022; Cram et al., 2024).

Its interpretation requires restraint. Amplicon sequencing normally reports relative rather than absolute abundance; taxonomic resolution can be insufficient to distinguish pathogenic and non-pathogenic strains; primer choice and DNA extraction introduce bias; and detection of bacterial DNA does not prove viability or virulence. Bui et al. (2026) found that 16S sequencing and flow-cytometric community fingerprints captured complementary aspects of microbial dynamics in commercial barramundi larviculture, reinforcing the value of combining rather than substituting methods.

3.4 Metagenomic and metatranscriptomic approaches

Shotgun metagenomics extends monitoring from marker genes to the broader genetic potential of a community. It can provide improved taxonomic resolution and detect genes related to metabolism, virulence, nutrient cycling, and antimicrobial resistance. In marine cage aquaculture, metagenomic analysis has revealed differences in both taxonomic composition and carbon-, nitrogen-, and sulfur-related functional profiles between aquaculture and nearby non-aquaculture waters (Liu et al., 2024). Such information may eventually help distinguish a harmless taxonomic shift from a functionally consequential one.

Metatranscriptomics adds another dimension by measuring expressed RNA and thus providing a closer view of microbial activity. Its practical barriers are cost, RNA instability, bioinformatic complexity, and the difficulty of separating biologically meaningful signals from short-term environmental responses. These approaches are therefore most valuable today for biomarker discovery and mechanistic research rather than routine monitoring of every production unit.

3.5 Multi-Omics approaches to microbial health monitoring

No single omics layer fully describes host–microbe–environment interactions. Metagenomics indicates functional potential, metatranscriptomics identifies active expression, metabolomics characterizes chemical outputs, and proteomics can reveal expressed proteins. Integrating these layers may therefore separate taxonomic change from functional change and identify mechanisms that would remain hidden in a 16S dataset alone.

This potential is illustrated by integrated metagenomic and metabolomic analysis of *Litopenaeus vannamei* exposed to microcystin-LR, where microbial functional shifts were examined together with altered intestinal metabolites (Duan et al., 2022). The study also illustrates a broader caution: multi-omics produces many associations, but candidate biomarkers still require experimental validation before becoming operational health indicators.

3.6 Rapid and on-site microbial detection technologies

Farm health decisions often require information faster than conventional sequencing can provide. Isothermal amplification, portable nucleic-acid platforms, biosensors, microfluidics, and high-throughput flow cytometry are attractive because they can reduce analytical turnaround. A LAMP assay developed for *Vibrio harveyi* demonstrated rapid target detection under isothermal conditions, and a more recent direct LAMP workflow for *V.*

parahaemolyticus was specifically tested with shrimp aquaculture water and designed around field deployment (Rahman et al., 2022; Pu et al., 2026).

Flow cytometry offers a different advantage: it rapidly measures phenotypic distributions of microbial cells without first knowing their taxonomy. Machine-learning analysis has shown that flow-cytometric fingerprints can contain information associated with bacterial community composition, although taxonomic abundance prediction remains imperfect (Heyse et al., 2021). In barramundi hatcheries, FCM and 16S sequencing showed complementary trends, suggesting a feasible future division of labor in which rapid fingerprints flag unusual community states and sequencing is reserved for diagnostic clarification (Figure 1) (Bui et al., 2026).

	Taxonomic breadth	Functional resolution	Quantification capability	Analytical speed	Field deployability	Operational complexity / cost
Culture-dependent methods	Low	Low	Medium	Medium	Low	Medium
qPCR / dPCR	Low	Low	High	High	Medium	Medium
16S rRNA sequencing	High	Medium	Medium	Medium	Low	High
Shotgun metagenomics	High	High	Medium	Low	Low	High
Multi-omics	High	High	Low	Low	Low	High
Flow cytometry (FCM)	Low	Low	Medium	High	High	Medium
LAMP / biosensors	Low	Low	Medium	High	High	Low

Low Medium High

Methods are complementary; no single platform is optimal for all monitoring purposes.

Figure 1 Comparison of major microbial monitoring technologies for marine aquaculture health management

4 Microbial Indicators for Health Assessment in Marine Aquaculture

4.1 Potential pathogenic microorganisms as risk indicators

Potential pathogens remain necessary indicators because an increasing pathogen burden can mark rising infection pressure. In marine aquaculture, *Vibrio*, *Photobacterium*, and *Tenacibaculum* are particularly relevant in many fish, shrimp, and shellfish contexts, while *Aeromonas* and other opportunistic genera are important in particular host and environmental settings. Long-term Sanggou Bay monitoring found seasonal enrichment of potentially pathogenic *Vibrio*, and experimental shrimp studies show that *Vibrio harveyi* exposure can restructure the gut community (Deris et al., 2022; Lu et al., 2025).

Nevertheless, genus-level detection alone is a weak diagnostic criterion. Different *Vibrio* lineages have sharply different ecological roles and virulence potential. Oyster hatchery monitoring provides a useful warning: *Vibrio* groups observed during some larval crashes appeared more likely to respond to deterioration than to initiate it (Cram et al., 2024). Pathogen surveillance should therefore combine abundance, species or strain identity where possible, virulence markers, host signs, and environmental context.

4.2 Beneficial and health-associated microorganisms

Positive indicators can be as informative as pathogens if they represent persistent organisms associated with a resilient host or culture environment. Candidate beneficial bacteria may suppress pathogens through competition, antimicrobial production, resource exclusion, or modification of the local environment. Roseobacter-group *Phaeobacter*, for example, has been studied as a probiotic candidate because some strains inhibit important aquaculture pathogens (Sonnenschein et al., 2021).

Yet "beneficial" should not become another taxonomic shortcut. Performance depends on strain, host, diet, dose, environment, and microbial community context. Dietary supplementation with *Pseudoalteromonas piscicida* and fructooligosaccharide has produced beneficial outcomes in experimental whiteleg shrimp, but such results do not justify classifying every *Pseudoalteromonas* as beneficial (Nababan et al., 2022). Positive indicators should therefore be validated at strain or function level and against defined production outcomes.

4.3 Microbial diversity and community stability

Diversity metrics are attractive because they compress complex communities into simple numbers, but their biological meaning is context dependent. A sudden diversity loss can accompany dysbiosis, yet high diversity is not automatically equivalent to health. Communities may naturally change during host development, system maturation, feed transitions, or seasonal shifts. Biofloc shrimp culture, for instance, shows substantial stage-dependent succession even during successful production (Kim et al., 2022).

Temporal stability, resilience after disturbance, and deviation from a farm-specific reference state may therefore be more useful than an isolated Shannon or Chao1 value. Clinton et al. (2024) found specific Atlantic salmon gill taxa associated with different health states even though general richness and diversity were not consistently related to pathology. This supports a multidimensional interpretation in which diversity is contextual evidence rather than a stand-alone diagnosis.

4.4 Microbial dysbiosis as an early-warning indicator

Dysbiosis is especially promising for early warning because disease may emerge from a broader ecological destabilization rather than a single pathogen crossing a universal threshold. Candidate warning signals include unusual community turnover, expansion of opportunists, disappearance of persistent taxa, loss of network complexity, and changed community functions. Reviews of aquaculture microbiomes identify these patterns as plausible biomarkers but emphasize their strong host and environmental dependence (Mougin and Joyce, 2023; Xavier et al., 2024).

The timing of dysbiosis is decisive. A useful warning indicator must change before irreversible host deterioration, not merely describe a sick animal. In oyster larvae, community structure at an early developmental stage showed associations with later batch performance, while many taxa appearing during crashes were probably secondary responders (Cram et al., 2024). This distinction argues strongly for dense longitudinal sampling in biomarker-discovery studies.

4.5 Functional microbial indicators

Functional markers may sometimes generalize better than specific taxa because similar ecological functions can be performed by different organisms. Potential examples include virulence genes, antimicrobial-resistance determinants, nitrogen-cycle genes, oxidative-stress responses, and metabolite-production pathways. Metagenomic surveys can therefore ask not only "who is present?" but also "what biological capabilities are becoming more or less abundant?" (Liu et al., 2024).

A practical monitoring system might eventually combine a small taxonomic panel with a functionally informative gene panel. This would be particularly valuable where strain-level pathogenicity differs within a genus. Functional indicators still require careful interpretation because gene presence does not prove expression, while metatranscriptomic or metabolomic activity can be transient. Their main advantage is thus mechanistic specificity, not automatic diagnostic certainty.

5 Major Factors Shaping Microbial Health in Marine Aquaculture

5.1 Water quality and environmental conditions

Microbial communities respond quickly to the physical and chemical environment. Temperature influences growth rates and seasonal succession; salinity filters taxa according to osmotic tolerance; dissolved oxygen affects aerobic and anaerobic processes; and pH, ammonia, nitrite, and organic matter alter both microbial metabolism and host stress. In Sanggou Bay, temperature, dissolved oxygen, and transparency were significantly associated with bacterioplankton dynamics and seasonal pathogen patterns (Lu et al., 2025).

These relationships are rarely linear or universal. Experimental shrimp work showed that salinity interacted with *V. harveyi* exposure to reshape gut-community structure and network properties (Deris et al., 2022). Monitoring schemes should consequently interpret microbial signals together with environmental trajectories rather than treating water chemistry and microbiology as separate data streams.

5.2 Stocking density and culture intensity

Higher culture intensity increases feed demand, waste production, host-to-host contact, and microbial exchange. These processes can stimulate heterotrophic growth and create niches for opportunistic organisms, particularly when oxygen supply or waste removal becomes limiting. The effect is not simply “high density causes disease”; management technology determines how biological loading is handled.

For this reason, microbial monitoring may be most useful when interpreted relative to biomass and production stage. The same bacterial density can have different meanings early and late in a production cycle. Longitudinal biofloc observations demonstrate that microbial succession accompanies increasing culture age and organic loading, suggesting that stage-specific reference ranges are preferable to one farm-wide threshold (Kim et al., 2022).

5.3 Feed and feeding management

Feed influences microbial health through two pathways. Consumed feed changes the intestinal chemical environment and substrate availability, while uneaten feed and fecal material enter the surrounding system and stimulate environmental microorganisms. The resulting changes can alter oxygen demand, nutrient transformations, biofilm growth, and microbial exchange between water and host.

Feed management should therefore be included in microbial interpretation even when it is not the primary research variable. Studies comparing aquaculture management systems show that environmental and intestinal microbiomes respond to production practices, including probiotic and biofloc approaches (Waiho et al., 2023). Future farm baselines should record major diet transitions and feeding-rate changes so that ordinary nutritional responses are not misclassified as disease warnings.

5.4 Water exchange, aeration, and system management

Water exchange and aeration alter microbial dispersal, oxygenation, particle suspension, and resource availability. Recirculating systems add biological filtration, creating engineered microbial niches that perform essential nitrification and other transformations. These microorganisms can also disperse between system water and animal surfaces, making the boundary between “environmental” and “host-associated” microbiota particularly porous.

Atlantic salmon raised in RAS showed temporal changes in skin, gill, and water microbiomes, including a period interpreted as possible dysbiosis that later recovered (Lorgen-Ritchie et al., 2022). In biofloc shrimp systems, microbial communities also changed markedly as the system matured (Kim et al., 2022). These observations favor adaptive baselines tailored to system design rather than comparisons with a supposedly universal marine microbiome.

5.5 Antibiotics, disinfectants, and other chemical interventions

Chemical disease control can alter non-target microorganisms as well as pathogens. This matters because treatment may temporarily suppress one pathogen while changing ecological niches, selecting resistant populations, or disrupting host-associated communities. In gilthead seabream, bacterial infection and subsequent oxytetracycline

treatment were accompanied by restructuring of skin, gill, and gut microbiomes, with tissue-specific changes in diversity and taxonomic composition (Rosado et al., 2023).

The appropriate conclusion is not that antimicrobial treatment should never be used, but that it should be justified diagnostically and accompanied by good biosecurity and follow-up monitoring. This aligns with international guidance emphasizing responsible antimicrobial use and resistance surveillance in aquatic animals. Microbiome recovery after treatment may itself become a useful future management endpoint.

5.6 Biological and microbial interventions

Probiotics, prebiotics, synbiotics, biofloc, and microbial consortia aim to steer microbial ecology rather than simply eliminate microorganisms. Their mechanisms can include competition with pathogens, production of inhibitory metabolites, stimulation of host immunity, and improved transformation of wastes. Research on *Phaeobacter* and other candidate probiotics provides a mechanistic basis for such approaches, while shrimp feeding experiments demonstrate that microbial and prebiotic combinations can influence disease resistance under controlled conditions (Sonnenschein et al., 2021; Nababan et al., 2022).

More ambitious strategies—microbiome transplantation, synthetic communities, and microbiome engineering—remain largely experimental in aquaculture. Their promise should not be confused with readiness for routine farm use. Ecological persistence, biosafety, host specificity, horizontal gene transfer, regulatory requirements, and unintended community effects all need evaluation before deliberate microbiome manipulation becomes a standard management practice.

6 Microbial Monitoring for Disease Risk Assessment and Early Warning

6.1 From pathogen detection to ecosystem-level health monitoring

A pathogen-centered test asks whether a particular agent is present. Ecosystem-level surveillance asks a broader question: is the biological system moving away from its normal operating state? The second approach incorporates environmental microbiota, host-associated microbiota, water quality, husbandry, and clinical observations. It does not weaken pathogen diagnostics; instead, it determines when targeted diagnostics should be intensified.

This shift is supported by evidence that aquaculture disease is often accompanied by community-wide restructuring. In shrimp, fish, and oysters, disease-associated microbial patterns extend beyond the nominal pathogen, while environmental conditions can strongly modify these patterns (Huang et al., 2020; Clinton et al., 2024). A useful surveillance hierarchy is therefore broad screening first, targeted confirmation second, and intervention only after biological context has been considered.

6.2 Microbial signatures associated with pre-disease states

The most valuable biomarker is not necessarily the organism most abundant in a diseased sample. From a management perspective, earlier and moderately predictive signals can be more useful than perfect post-disease classification. Oyster hatchery observations are instructive because microbial differences were detectable before later production failure, whereas several organisms that dominated during crashes appeared to be consequences of deteriorating host condition (Cram et al., 2024).

This temporal requirement changes experimental design. Cross-sectional comparisons of “healthy” and “diseased” animals are valuable for generating hypotheses, but they cannot reliably determine whether microbial change precedes pathology. Longitudinal studies that repeatedly sample the same production units, record host outcomes, and retain environmental metadata are more appropriate for discovery of genuine early-warning signals. Recent commercial barramundi monitoring further demonstrates that even nominally similar tanks can develop distinct microbial trajectories, so replication at the tank level is essential (Bui et al., 2026).

6.3 Integration of microbial and environmental indicators

Microbial data become operationally meaningful when linked to conditions that farmers can observe or modify. A rising opportunistic-pathogen signal has different implications under stable temperature and oxygen than during

rapid warming, hypoxia, or deteriorating nitrogen conditions. Integrating these measurements can therefore distinguish random microbial fluctuation from an ecological transition with plausible biological consequences.

Sanggou Bay provides a field-scale example: seasonal bacterial restructuring and potentially pathogenic *Vibrio* patterns were analyzed alongside physicochemical variables rather than interpreted in isolation (Lu et al., 2025). The practical lesson is simple. A health dashboard should not contain "microbiome" as a separate compartment; microbial, environmental, husbandry, and host data should be treated as interacting dimensions of the same production system.

6.4 Microbial health risk classification

A three-level classification offers a practical way to translate continuous microbial variation into management decisions. The categories below are conceptual rather than validated universal thresholds. Numerical cutoffs should only be established after longitudinal calibration for a specific species, farm, production stage, sample type, and analytical method (Table 1).

Level I: Healthy

At this level, microbial measurements remain within an established farm- and stage-specific baseline. Potential pathogens are absent, low, or stable relative to historical observations; community turnover follows expected seasonal or developmental trajectories; environmental parameters remain acceptable; and animals show normal feeding, behavior, and survival. Routine monitoring continues without unnecessary intervention.

Level II: Alert

An alert should be triggered by convergence rather than one isolated result. Examples include repeated increases in an opportunistic pathogen, unexpected community displacement, reduced stability, disappearance of persistent health-associated taxa, or environmental stress occurring at the same time as microbial change. Sampling frequency should increase, the signal should be confirmed by an independent or targeted method, and modifiable husbandry factors should be reviewed before disease becomes clinically evident.

Level III: High Risk

High risk is characterized by multiple lines of evidence suggesting loss of system resilience: substantial pathogen enrichment or virulence-marker detection, persistent dysbiosis, unfavorable environmental change, and early host-health abnormalities. At this point, farm biosecurity and diagnostic procedures should be escalated, affected production units assessed separately, and any therapeutic intervention based on appropriate veterinary and laboratory evidence rather than microbiome data alone.

Table 1 Conceptual microbial indicators and corresponding management responses. These signals are intended for farm-specific calibration; they are not universal diagnostic thresholds

Indicator domain	Routine/healthy pattern	Alert or high-risk signal	Management interpretation and action
Target pathogens	Stable low background or non-detection	Repeated increase; virulence marker confirmed	Re-sample; confirm with qPCR/dPCR or culture; strengthen diagnostics and biosecurity
Community structure	Expected seasonal/developmental variation	Abrupt or persistent deviation from baseline	Increase monitoring; examine recent husbandry and environmental changes
Diversity/stability	Farm-specific normal range	Sudden loss of stability or resilience	Treat as supporting evidence, not diagnosis by itself
Health-associated taxa	Persistent baseline pattern	Repeated decline or disappearance	Examine concurrent stressors; avoid assuming causality without validation
Functional genes	Stable functional profile	Enrichment of virulence, stress, or resistance functions	Confirm target identity/activity; review antimicrobial and biosecurity history
Water quality	Expected operational range	Warming, hypoxia, nitrogen stress, organic loading	Correct manageable environmental stress and assess interaction with microbial signal
Host condition	Normal feeding, behavior and survival	Reduced feeding, lesions, abnormal behavior, increased mortality	Escalate clinical/pathogen diagnostics and targeted intervention

The value of the table is not the creation of fixed thresholds but the linkage of microbial evidence to progressively stronger actions. Such proportionality reduces two opposite errors: ignoring early ecological deterioration and overreacting to ordinary microbiome variability. Evidence from longitudinal aquaculture studies strongly supports this need for contextual rather than single-marker interpretation (Clinton et al., 2024; Lu et al., 2025).

6.5 Data-driven approaches for microbial risk prediction

Multivariate statistics and machine learning are well suited to microbial monitoring because the number of candidate microbial features often far exceeds the number of samples. Random forests, regularized regression, time-series models, and neural networks can combine taxa, cytometric features, environmental variables, and host measurements. Flow-cytometry research has already shown that microbial fingerprints contain enough structure to predict aspects of taxonomic composition, supporting their potential role in rapid screening (Heyse et al., 2021).

The main constraint is not algorithm availability but data quality. Models trained on one farm, season, or analytical pipeline may learn local signatures that fail elsewhere. Tank-level replication, independent validation, temporal testing, transparent feature selection, and calibrated uncertainty are therefore more important than model complexity. For current aquaculture applications, interpretable models that show why a sample was classified as risky may be more useful than opaque systems with marginally higher internal accuracy (Figure 2).

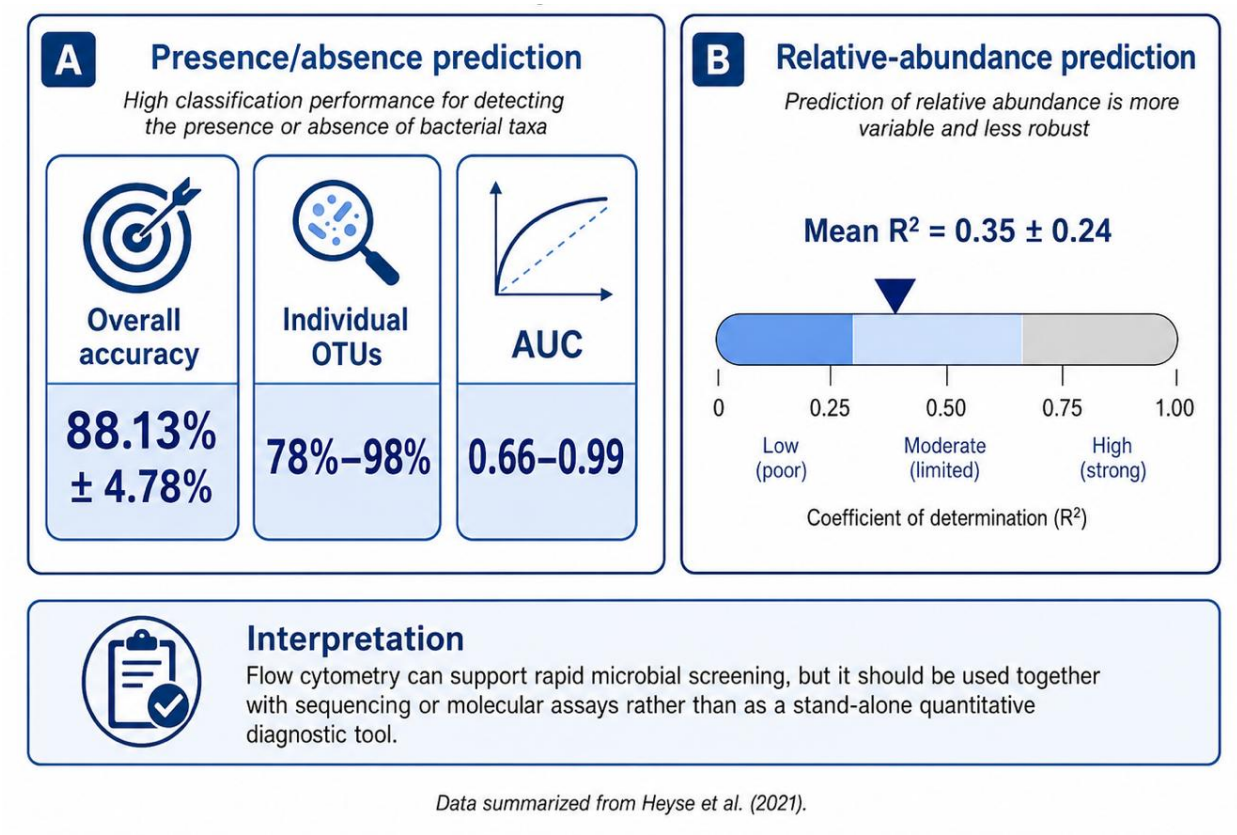

Figure 2 Performance of flow cytometry-based prediction of bacterial taxa in an aquaculture microbial community

7 Microbial Monitoring-Based Health Management Models for Marine Aquaculture

7.1 Routine microbial surveillance model

Routine surveillance begins by establishing what "normal" looks like. This requires repeated sampling during periods of acceptable production, covering major seasons, developmental stages, and management transitions. Baselines should include a manageable set of microbial measures-such as total cell counts, targeted pathogen abundance, community fingerprints, or periodic 16S profiles-alongside temperature, salinity, dissolved oxygen, nitrogen compounds, feeding, biomass, and health records.

Importantly, the baseline is a distribution, not a single reference sample. Longitudinal studies repeatedly demonstrate natural microbial succession in aquaculture systems (Kim et al., 2022; Bui et al., 2026). A farm that samples only during disease events has no reliable ecological reference against which to judge those events. Routine surveillance is therefore the foundation on which all later warning thresholds depend.

7.2 Microbial early-warning management model

Early-warning management focuses on deviation rather than diagnosis. A rapid monitoring tool might first identify an unusual cell-density pattern, pathogen increase, or community fingerprint. The result should then trigger confirmation using a more specific method and a simultaneous review of environmental and host data. This layered strategy balances speed with diagnostic reliability.

The approach is particularly attractive in hatcheries because microbial conditions can change quickly and early life stages are often vulnerable. Findings from oyster and barramundi larviculture suggest that community trajectories contain information related to later performance, although the predictive signals are not yet universal (Cram et al., 2024; Bui et al., 2026). Early warning should consequently be framed as increased probability requiring attention, not as certainty that disease will occur.

7.3 Risk-based intervention model

A risk-based model links intervention intensity to the weight of evidence. Low-risk conditions require routine husbandry; alert conditions justify increased sampling and correction of obvious environmental stress; high-risk conditions require focused diagnostic and biosecurity responses. Where intervention is necessary, management may include adjustment of feeding, aeration, water exchange, system hygiene, movement of animals, or other measures appropriate to the culture system.

This model also discourages prophylactic antimicrobial use based solely on a nonspecific microbial shift. Antimicrobials can themselves disrupt microbiomes, while responsible use is important for limiting resistance selection (Rosado et al., 2023). A microbiome-informed system should therefore reduce diagnostic uncertainty rather than create a new reason for indiscriminate treatment.

7.4 Microbiome regulation-based health management

Once a reproducible adverse microbial state has been identified, management can move beyond observation toward ecological regulation. Probiotics, prebiotics, synbiotics, biofloc management, and carefully selected microbial consortia are plausible tools for maintaining competitive microbial communities and improving host resilience. Evidence for *Phaeobacter* and other probiotic candidates shows that antagonism against pathogens can be harnessed, although effects remain strain- and system-dependent (Sonnenschein et al., 2021).

A more sophisticated goal is restoration of microbial function rather than introduction of one “beneficial” species. That idea remains ahead of current commercial evidence. Synthetic consortia, microbiota transplantation, and targeted microbiome engineering will require ecological and biosafety validation, especially in open marine systems where introduced microorganisms can interact with natural communities.

7.5 Adaptive and feedback-based health management

Health management becomes adaptive when monitoring does not end after intervention. Post-intervention samples should determine whether pathogen abundance decreased, microbial structure returned toward its normal range, environmental stress was corrected, and host condition improved.

7.6 Toward precision health management in marine aquaculture

Precision management requires thresholds that are specific enough to the farm to be meaningful but standardized enough to be transferable and audited. A practical future architecture may combine continuous environmental sensors with frequent low-cost microbial screening, less frequent sequencing for baseline renewal, and targeted molecular assays when warning signals appear.

Such a system does not require sequencing every sample. Indeed, an economically realistic workflow may use high-information technologies during discovery, then translate validated biomarkers into qPCR, dPCR, flow-cytometric, or biosensor assays. The recent development of field-oriented LAMP and rapid microbial fingerprinting supports this two-stage model of discovery followed by operational simplification (Pu et al., 2026; Bui et al., 2026).

8 Applications Across Major Marine Aquaculture Systems

8.1 Marine finfish aquaculture

Finfish provide multiple microbiome compartments for health monitoring, including water, gut, gills, skin, and mucus. External mucosae are particularly informative because they directly experience environmental change while functioning as barriers to infection. In marine-stage Atlantic salmon, specific gill-associated taxa correlated with gill-health status over a year-long production cycle, although general diversity metrics were not sufficient to define health (Clinton et al., 2024).

Gilthead seabream research also demonstrates that infection and antimicrobial treatment can affect different mucosal microbiomes in distinct ways (Rosado et al., 2023). Marine finfish monitoring should therefore avoid assuming that gut samples alone represent whole-animal microbial health. A tissue-specific sampling strategy is more defensible when the disease of interest has a defined portal of entry or mucosal target.

8.2 Shrimp aquaculture

Shrimp farming is particularly suited to microbial surveillance because animals and environmental microorganisms are closely connected through water, sediment, feed, fecal material, and the intestinal tract. Studies in *L. vannamei* have documented developmental changes in intestinal microbiota, salinity-associated restructuring, disease-related dysbiosis, and microbial differences among clear-water, probiotic, and biofloc production approaches (Deris et al., 2022; Vinay et al., 2022; Waiho et al., 2023).

Vibrio monitoring remains important, but its interpretation should extend beyond total relative abundance. Species, virulence potential, absolute load, environmental stress, and broader community structure provide a more defensible assessment. Shrimp studies of dysbiosis also show why community-level signals may complement rather than replace specific pathogen testing (Huang et al., 2020).

8.3 Shellfish aquaculture

Shellfish hatcheries illustrate both the promise and difficulty of microbial prediction. Larval cultures can undergo rapid production failure, yet potential pathogens may not always be the primary trigger. Cram et al. (2024) found that early microbial-community patterns in oyster larvae were related to later batch outcomes, while several organisms enriched during crashes likely took advantage of already deteriorating conditions.

Pacific oyster mortality syndrome provides a further example of complex disease ecology in which viral infection, bacterial communities, host susceptibility, and environment interact. Experimental work has associated microbiota composition with different disease outcomes, supporting the idea that shellfish health may need to be understood as a pathobiome rather than a one-pathogen system (Delisle et al., 2022).

8.4 Recirculating and high-density marine aquaculture systems

Engineered systems provide unusually strong opportunities for microbial health management because water flows, biofilters, aeration, disinfection, and feeding are more controllable than in open-water culture. They also create complex microbial connectivity among water, biofilms, filters, and animal mucosae. Temporal Atlantic salmon RAS research demonstrates that substantial microbial restructuring can occur even in highly controlled production environments (Lorgen-Ritchie et al., 2022).

This controllability makes RAS suitable for testing causal management interventions. When a microbial warning appears, managers can modify operational variables and observe subsequent microbial responses. Over time, such feedback-rich systems could become test beds for validating health indicators before similar concepts are transferred to less controllable cage or coastal farms.

9 Challenges and Future Perspectives

9.1 Lack of standardized microbial health indicators

The largest conceptual obstacle is the absence of a universal microbial definition of health. Species identity, developmental stage, diet, tissue, salinity, geographic location, season, and farm design all influence microbiome composition. Reviews of aquaculture dysbiosis consistently find recurring patterns, such as pathogen enrichment and community restructuring, but not a single taxonomic profile that defines healthy fish across systems (Mougin and Joyce, 2023; Xavier et al., 2024).

Standardization should therefore focus first on measurement and interpretation rather than universal taxa. Comparable sampling procedures, metadata, controls, sequence processing, absolute abundance measurements, and outcome definitions would make it easier to identify indicators that genuinely transfer across farms.

9.2 Relative abundance versus absolute quantification

Amplicon sequencing is compositional. If one organism expands strongly, the apparent relative abundance of all other organisms may decline even when their absolute cell numbers remain unchanged. This makes relative abundance alone potentially misleading for health decisions.

Combining community sequencing with total-cell measurements, spike-in standards, qPCR, or digital PCR can address part of this problem. Digital PCR is particularly attractive for operational biomarkers because it provides absolute target quantification, while viability treatments can further distinguish viable-cell signals in some applications (Yang et al., 2023). Future health indices should report absolute microbial loads whenever the biological question concerns infection pressure rather than community composition alone.

9.3 From association to causality

A dysbiotic microbiome may be a cause of disease, a consequence of disease, or a correlated response to the same environmental stressor. Distinguishing these possibilities requires temporal and experimental evidence. Shrimp research using microbiota manipulation has provided unusually strong evidence that dysbiosis can contribute to disease processes, but such causal demonstrations remain far less common than cross-sectional associations (Huang et al., 2020).

Future biomarker development should therefore proceed in stages: longitudinal association, independent replication, mechanistic testing, and finally prospective prediction. Organisms identified only because they dominate moribund animals should not be promoted immediately as early-warning biomarkers.

9.4 Need for long-term and multi-farm monitoring

A model that performs well on samples from one farm may simply recognize that farm. Seasonal patterns can create the same problem: an algorithm may inadvertently learn sampling date rather than disease risk. The Sanggou Bay study demonstrates how strong seasonality can be relative to culture-mode effects, while barramundi hatchery observations reveal persistent differences among tanks managed within the same facility (Lu et al., 2025; Bui et al., 2026).

Robust validation therefore requires several production cycles, multiple farms, independent cohorts, and deliberately separated training and test data. Shared longitudinal datasets linking microbiomes with environmental variables and standardized health outcomes would probably advance the field more than increasingly complex algorithms trained on small local datasets.

9.5 Standardization and cost reduction

Differences in filtration volume, sample storage, DNA extraction, primer choice, sequencing depth, bioinformatic pipelines, and taxonomic databases can all change the apparent microbiome. Operational monitoring adds further constraints: methods must be fast, reproducible, affordable, and usable by non-specialist personnel.

One realistic route is a two-tier technology system. Research laboratories could use sequencing and multi-omics to discover and validate indicators, while farms employ simplified qPCR, dPCR, flow-cytometry, LAMP, or biosensor

panels. The emergence of direct LAMP workflows for shrimp-culture water illustrates how eliminating complex DNA extraction can materially improve field practicality (Pu et al., 2026).

9.6 Integration of multi-omics, artificial intelligence, and smart aquaculture

The strongest future prediction systems are likely to combine microbial and non-microbial data. Environmental sensors can continuously measure variables such as temperature, dissolved oxygen, pH, and salinity, whereas microbial sampling provides biological information that sensors cannot. Multi-omics can identify functionally meaningful features, and machine learning can integrate heterogeneous variables across time.

The risk is technological excess. More variables and more complex models do not guarantee better management. Flow-cytometry studies demonstrate both the promise and limits of data-driven microbial fingerprints: community information can be predicted rapidly, but accuracy differs among taxa and tasks (Heyse et al., 2021). Future smart-aquaculture systems should therefore prioritize external validation, interpretability, uncertainty estimates, and actionable outputs over algorithmic novelty.

9.7 From microbial monitoring to microbiome management

The long-term direction of the field is a transition from observing microbial communities to deliberately maintaining desirable ecological functions. In the near term, this means avoiding unnecessary disturbance, maintaining stable environmental conditions, using validated probiotics where appropriate, and recognizing microbial deterioration before clinical disease. More advanced interventions may eventually include precision probiotics, defined microbial consortia, phage-based strategies, and ecological engineering of water and biofilms.

That transition should remain evidence-led. Marine aquaculture systems are connected to wider coastal ecosystems, so interventions that alter microbial communities may have consequences beyond the farm boundary. The most defensible health-management model is therefore not one that attempts to control every microorganism, but one that combines surveillance, ecological understanding, proportional intervention, and learning from repeated production cycles. In this framework, the practical endpoint of microbial monitoring is neither sequencing nor pathogen enumeration. It is better timing of management: recognizing instability while it is still reversible, confirming risk before acting, and evaluating whether intervention restores both animal health and microbial resilience.

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